Emek Demir

List of Publications by Year
in descending order

58 papers	6,787 citations	147801 31 h-index	133252 59 g-index
78 all docs	78 docs citations	78 times ranked	9494 citing authors

#	Article	IF	Citations
1	The reactome pathway knowledgebase 2022. Nucleic Acids Research, 2022, 50, D687-D692.	14.5	924
2	An omic and multidimensional spatial atlas from serial biopsies of an evolving metastatic breast cancer. Cell Reports Medicine, 2022, 3, 100525.	6.5	22
3	Newt: a comprehensive web-based tool for viewing, constructing and analyzing biological maps. Bioinformatics, 2021, 37, 1475-1477.	4.1	24
4	An expanded universe of cancer targets. Cell, 2021, 184, 1142-1155.	28.9	135
5	Systematic interrogation of mutation groupings reveals divergent downstream expression programs within key cancer genes. BMC Bioinformatics, 2021, 22, 233.	2.6	1
6	Ribavirin shows antiviral activity against SARS-CoV-2 and downregulates the activity of TMPRSS2 and the expression of ACE2 in vitro. Canadian Journal of Physiology and Pharmacology, 2021, 99, 449-460.	1.4	41
7	2D MXenes with antiviral and immunomodulatory properties: A pilot study against SARS-CoV-2. Nano Today, 2021, 38, 101136.	11.9	63
8	Causal interactions from proteomic profiles: Molecular data meet pathway knowledge. Patterns, 2021, 2, 100257.	5.9	44
9	The AML microenvironment catalyzes a stepwise evolution to gilteritinib resistance. Cancer Cell, 2021, 39, 999-1014.e8.	16.8	62
10	COVID19 Disease Map, a computational knowledge repository of virus–host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	7.2	53
11	A flexible search system for high-accuracy identification of biological entities and molecules. Journal of Open Source Software, 2021, 6, 3756.	4.6	1
12	Analyzing causal relationships in proteomic profiles using CausalPath. STAR Protocols, 2021, 2, 100955.	1.2	7
13	Author-sourced capture of pathway knowledge in computable form using Biofactoid. ELife, 2021, 10, .	6.0	11
14	3024 – GERMLINE RUNX1 MUTATIONS -MEDIATED CHANGES COOPERATES WITH INFLAMMATORY MICROENVIRONMENT TO DRIVE DEFECTIVE HEMATOPOIESIS IN FAMILIAL PLATELET DISORDER. Experimental Hematology, 2021, 100, S55.	0.4	0
15	Pathway Commons 2019 Update: integration, analysis and exploration of pathway data. Nucleic Acids Research, 2020, 48, D489-D497.	14.5	161
16	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. Scientific Data, 2020, 7, 136.	5.3	99
17	Phosphoproteomic quantitation and causal analysis reveal pathways in GPVI/ITAM-mediated platelet activation programs. Blood, 2020, 136, 2346-2358.	1.4	53
18	Proteogenomic Characterization of Endometrial Carcinoma. Cell, 2020, 180, 729-748.e26.	28.9	296

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19	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	28.9	334
20	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	7.2	178
21	Cancer-associated mutations in DICER1 RNase IIIa and IIIb domains exert similar effects on miRNA biogenesis. Nature Communications, 2019, 10, 3682.	12.8	48
22	Systems Biology Graphical Notation: Process Description language Level 1 Version 2.0. Journal of Integrative Bioinformatics, 2019, 16, .	1.5	43
23	Large-scale automated machine reading discovers new cancer-driving mechanisms. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	40
24	Platelet procoagulant phenotype is modulated by a p38-MK2 axis that regulates RTN4/Nogo proximal to the endoplasmic reticulum: utility of pathway analysis. American Journal of Physiology - Cell Physiology, 2018, 314, C603-C615.	4.6	18
25	Assessment of roles for the Rho-specific guanine nucleotide dissociation inhibitor Ly-GDI in platelet function: a spatial systems approach. American Journal of Physiology - Cell Physiology, 2017, 312, C527-C536.	4.6	21
26	Human SRMAtlas: A Resource of Targeted Assays to Quantify the Complete Human Proteome. Cell, 2016, 166, 766-778.	28.9	295
27	PaxtoolsR: pathway analysis in R using Pathway Commons. Bioinformatics, 2016, 32, 1262-1264.	4.1	43
28	Systems Biology Graphical Notation: Process Description language Level 1 Version 1.3. Journal of Integrative Bioinformatics, 2015, 12, 213-280.	1.5	15
29	Systems Biology Graphical Notation: Activity Flow language Level 1 Version 1.2. Journal of Integrative Bioinformatics, 2015, 12, 340-381.	1.5	35
30	Promoting Coordinated Development of Community-Based Information Standards for Modeling in Biology: The COMBINE Initiative. Frontiers in Bioengineering and Biotechnology, 2015, 3, 19.	4.1	72
31	Crosstalk between Signaling Pathways Provided by Single and Multiple Protein Phosphorylation Sites. Journal of Molecular Biology, 2015, 427, 511-520.	4.2	47
32	Systematic identification of cancer driving signaling pathways based on mutual exclusivity of genomic alterations. Genome Biology, 2015, 16, 45.	8.8	145
33	SBGNViz: A Tool for Visualization and Complexity Management of SBGN Process Description Maps. PLoS ONE, 2015, 10, e0128985.	2.5	26
34	Perturbation biology nominates upstream–downstream drug combinations in RAF inhibitor resistant melanoma cells. ELife, 2015, 4, .	6.0	95
35	Prediction of individualized therapeutic vulnerabilities in cancer from genomic profiles. Bioinformatics, 2014, 30, 2051-2059.	4.1	30
36	Pattern search in BioPAX models. Bioinformatics, 2014, 30, 139-140.	4.1	45

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37	Integrating biological pathways and genomic profiles with ChiBE 2. BMC Genomics, 2014, 15, 642.	2.8	24
38	The BioPAX Validator. Bioinformatics, 2013, 29, 2659-2660.	4.1	9
39	Using Biological Pathway Data with Paxtools. PLoS Computational Biology, 2013, 9, e1003194.	3.2	57
40	1P271 Crosstalk between signaling pathways revealed by database analysis of human phosphorylation sites(22B. Bioinformatics: Functional genomics,Poster). Seibutsu Butsuri, 2013, 53, S150.	0.1	0
41	Software support for SBGN maps: SBGN-ML and LibSBGN. Bioinformatics, 2012, 28, 2016-2021.	4.1	74
42	BioPAX support in CellDesigner. Bioinformatics, 2011, 27, 3437-3438.	4.1	18
43	Systems Biology Graphical Notation: Process Description language Level 1. Nature Precedings, 2011, , .	0.1	12
44	LibSBGN: Electronic Processing of SBGN maps. Nature Precedings, 2011, , .	0.1	0
45	Systems Biology Graphical Notation: Entity Relationship language Level 1 (Version 1.2). Nature Precedings, 2011, , .	0.1	5
46	Meeting report from the first meetings of the Computational Modeling in Biology Network (COMBINE). Standards in Genomic Sciences, 2011, 5, 230-242.	1.5	7
47	Pathway Commons, a web resource for biological pathway data. Nucleic Acids Research, 2011, 39, D685-D690.	14.5	980
48	The BioPAX community standard for pathway data sharing. Nature Biotechnology, 2010, 28, 935-942.	17.5	613
49	LibSBGN: Electronic Processing of SBGN maps. Nature Precedings, 2010, , .	0.1	0
50	Automated Network Analysis Identifies Core Pathways in Glioblastoma. PLoS ONE, 2010, 5, e8918.	2.5	318
51	Discovering modulators of gene expression. Nucleic Acids Research, 2010, 38, 5648-5656.	14.5	34
52	ChiBE: interactive visualization and manipulation of BioPAX pathway models. Bioinformatics, 2010, 26, 429-431.	4.1	46
53	Algorithms for effective querying of compound graph-based pathway databases. BMC Bioinformatics, 2009, 10, 376.	2.6	25
54	The Systems Biology Graphical Notation. Nature Biotechnology, 2009, 27, 735-741.	17.5	828

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55	A layout algorithm for undirected compound graphs. Information Sciences, 2009, 179, 980-994.	6.9	74
56	PATIKAmad: Putting microarray data into pathway context. Proteomics, 2008, 8, 2196-2198.	2.2	8
57	A Compound Graph Layout Algorithm for Biological Pathways. Lecture Notes in Computer Science, 2005, , 442-447.	1.3	12
58	Systems Biology Graphical Notation: Entity Relationship language Level 1 (Version 1.2). Nature Precedings, 0, , .	0.1	2